Amino Acid Sequence of EGIII

MKFLQVLPALIPAALAQTSCDQWATFTGNGYTVSNNLWGASAGSGFGCVTAVSLSGGAHADW
QWSGGQNNVKSYQNSQIAIPQKRTVNSISSMPTTASWSYSGSNIRANVAYDLFTAANPNHVT
YSGDYELMIWLGKYGDIGPIGSSQGTVNVGGQSWTLYYGYNGAMQVYSFVAQTNTTNYSGDV
KNFFNYLRDNKGYNAAGQYVLSYQFGTEPFTGSGTLNVASWTASIN

FIGURE 1

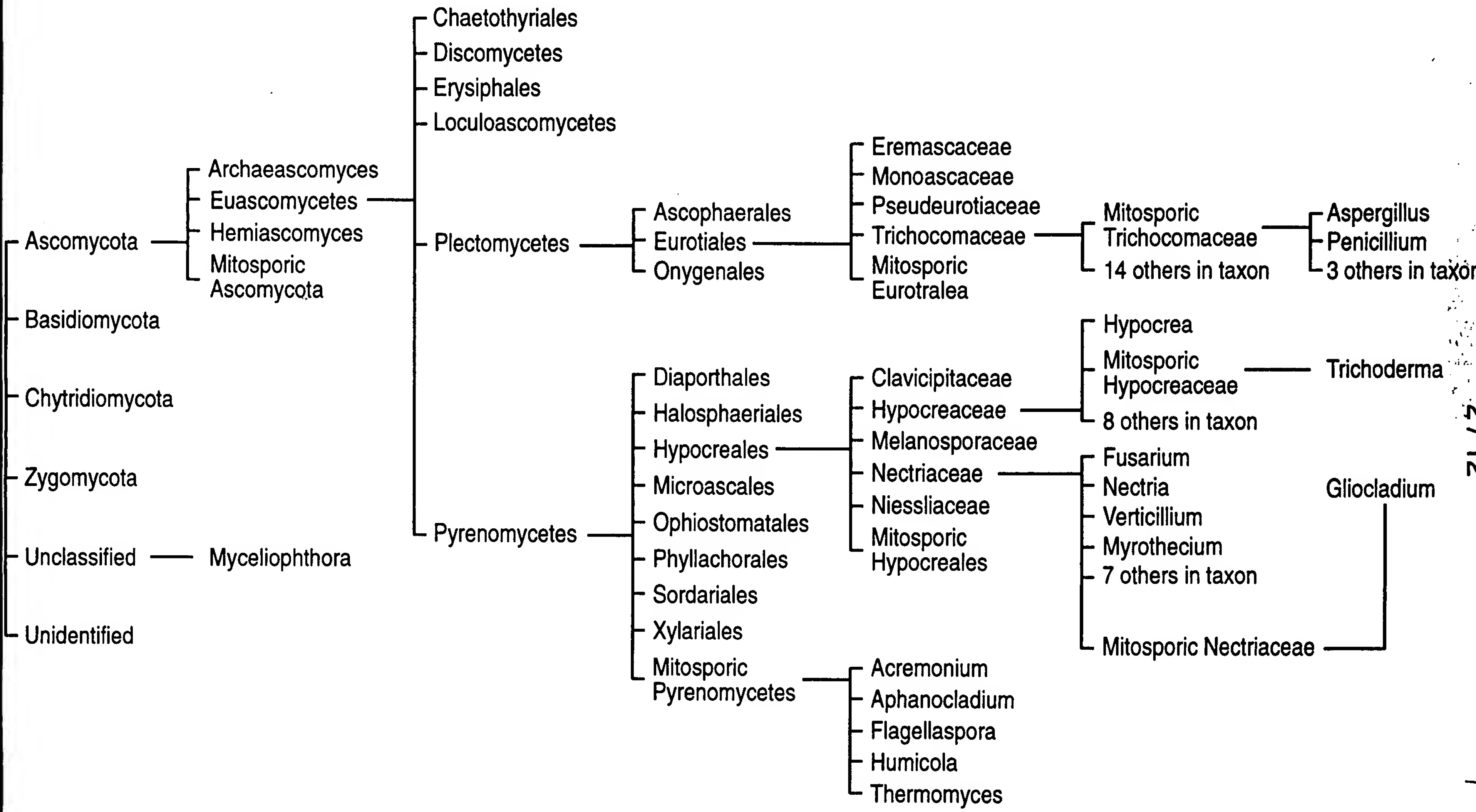

FIG._2


NNLWGKDSG--GSQCTTVDSLSDGGI-SWSTAWSWSGGEGNVKSYPNS------GLQFSAGKK-VSSISS
10 20 30 40 50 60 70
EG3IN.PRO NNLWGASAGS-GFGCVTAVSLSG-GA-SWHADWQWSGGQNNVKSYQNS------QIAIPQ-KRTVNSISS 60
FUSEQIN.PRO NNFWGKDSGT-GDQCTHVNWNNANGA-GWDVEWNWSGGKDNVKSYPNS------ALLIGEDKKTISSITN 62
GLIOIN.PRO NNKWGQGSGS-GSQCLTIDKIWDSNV-AFHADWSWSGGTNNVKSYPKR------RSEFSRGKK-VSSIGT 61
ACRHYPO.PRO ---WGPRSAESGEQCTTNNGLSDDGTLSWSVEWIWVGAPSSVKSYPN--------VFVEAEPRPLSEVSS 59
ASPKAWA1.PRO QNLWGEYQGT-GSQCVYVDKLSSSGA-SWHTKWIWSGGEGTVKSYSNS------GLTF-D-KKLVSDVSS 60
ASPACU1.PRO NNLWGKDAGS-GSQCTTVNSASSAGT-SWSTKWNWSGGENSVKSYANS------GLTF-N-KKLVSQISQ 60
HUMIN.PRO NNLWGKDTATSGWQCTYLDGTNNGGI-QWSTAWEWQGAPDNVKSYPYV------GKQIQRGRK-ISDINS 62
11AG8IN.PRO NNRWGTSAT----QC----INVTGNGFEITQADGSVPTNGAPKSYPSVYDGCHYGNC-APRTTLPMRISS 61
ERWCARIN.PRO NNVWGKDEI----KG-WQQTIFYNSPISMGWNWHWPSSTHSVKAYPSLVSGWHWTAGYTENSGLPIQLSS 65
GLIO314.PRO NNLWGMGSGS-GSQCTYVDKVWAEGV-AWHTDWSWSGGDNNVKSYPYS------GRELGTKRI-VSSIKS 61
GLIO3HYP.PRO NNLWGQDNG-SGSQCLTVEGVTDGLA-AWSSTWSWSGGSSSVKSYSNA------VLSAEAAR--ISAISS 60
HGRIS.PRO NNLWGQDTATSGWQCTYLDGTNNGGI-QWSTAWEWQGAPDNVKSYPYV------GKQIQRGRK-ISDINS 62
RHMARIN.PRO NNVWGAETA----QC--IEVGLETGNFTITRADH--DNGNNVAAYPAIYFGCHWAPARAIRDCAARAGAV 62
SLIVIN.PRO NNRWGSTAP----QC----VTATDTGFRVTQADGSAPTNGAPKSYPSVFNGCHYTNC-SPGTDLPVRLDT 61
PENNOT.PRO ---WGKDSGS-GSQCASVNSISDSGV-SWSTTWNWSGGEDNVKSYPNS------GLVALK-KQPVSDISS 58
PHANHYPO.PRO ---WGKDSG-TGSQCLTVDGISSGLL-KWSATWSWSGGPYNVKSYPNA------VLQAPAAR--ASAISS 57
F42HYPO.PRO -----S--------QCTTFESLSGNTI-VWNTKWSWSGGQGQVKSFANA------ALQFTPKK--LSSVKS 49
EMDESHYP.PRO NNLWGXDNADSGSQCTGVDSANGNSI-SWHTTWSWSGGSSSVKSYANA------AYQFTSTK--LNSLSS 61
MYCINS.PRO ---------- 1
CHBRAS.PRO NNFWGQSRATSGSQCTYLDSSSNSGI-HWHTTWIWEGGEGEVKSYAYS------GRQVSTGLT-IASIDS 62
IPSSASWV-YSGTDIRA-NVAYDL-FTAADPNHATSSGDYELMIW
80 90 100 110
EG3IN.PRO MPTTASWS-YSGSNIRA-NVAYDL-FTAANPNHVTYSGDYELMIW 102
FUSEQIN.PRO MQSTAEWK-YSGDNLRA-DVAYDL-FTAADPNHETSSGEYELMIW 104
GLIOIN.PRO INGGADWD-YSGSNIRA-NVAYGI-FTSADPNHVTSSGDYELMIW 103
ACRHYPO.PRO IQAEWAWTYSGAGDFTT-NVAFDI-FTGETAD 89
ASPKAWA1.PRO IPTSVTWS-QDDTNVQA-DVSYDL-FTAANADHATSSGDYELMIW 102
ASPACU1.PRO IPTTARWS-YDNTGIRA-DVAYDL-FTAADINHVTWSGDYELMIW 102
HUMIN.PRO MRTSVSWT-YDRTDIRA-NVAYDV-FTARDPDHPNWGGDYELMIW 104
11AG8IN.PRO IGSAPSSVSYRYTGNGVYNAAYDIWLDPTPRTNGVNR--TEIMIW 104
ERWCARIN.PRO NKSITSNVTYSIKATGTYNAAYDIWFHTTDKANWDSSPTDELMIW 110
GLIO314.PRO ISSGADWD-YTGSNLRA-NAAYDI-FTSANPNHATSSGDYELMIW 103
GLIO3HYP.PRO IPSKWEWRSYTGTDIVA-NVAYDL-FSNTDCGDTP---EYELMIW 100
HGRIS.PRO MRTSVSWT-YDRTDIRA-NVAYDV-FTARDPDHPNWGGDYEFMIW 104
RHMARIN.PRO RRAHELDVT-PI-TTGRWNAAYDIWFSPVTNSGNGYSGGAELMIW 105
SLIVIN.PRO VSAAPSSISYGFVDGAVYNASYDIWLDPTARTDGVNQ--TEIMIW 104
PENNOT.PRO IPSSVKWN-YDNTDIRA-DVAYDL-FTAADINHDTSSGDYE 96
PHANHYPO.PRO IPSKWQWESYTGSNVIA-NVAYDL-FSNSDCG 87
F42HYPO.PRO IDSTWKWKSYSGSNIVA-DVAYDM-FLSTSPGGDH---NY 84
EMDESHYP.PRO IPTSWKWQ-YSTTDIVA-NVAYDL-FTSSSAGGDS---EYEFMIW 100
MYCINS.PRO ----------A-NVAYDL-FTAADPNHATSSGDYELMIW 27
CHBRAS.PRO MQTSVSWE-YNTTDIQA-NVAYDI-FTAEDPDHEHSSGDYELMIW 104

FIGURE 3

Percent Similarity

Percent Divergence

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	
1		51.0	52.9	27.0	49.0	56.9	43.1	17.6	18.6	55.9	37.0	42.2	16.7	14.7	50.0	39.1	36.9	36.0	88.9	46.1	1
2	43.1		48.5	22.5	47.1	55.9	43.3	15.4	21.2	54.4	37.0	41.3	15.4	13.5	55.2	40.2	34.5	34.0	88.9	42.3	2
3	42.6	48.5		21.3	42.2	49.0	41.7	15.5	22.3	68.9	38.0	41.7	16.5	12.6	50.0	40.2	34.5	33.0	85.2	44.7	3
4	66.7	66.3	70.6		25.8	31.5	31.5	18.0	20.2	22.5	34.8	31.5	12.4	16.9	28.1	33.3	28.6	33.7	22.2	29.2	4
5	44.6	51.0	53.5	63.1		65.7	40.2	12.7	22.5	51.0	38.0	39.2	11.8	12.7	59.4	41.4	36.9	40.0	81.5	49.0	5
6	36.6	41.2	46.5	61.9	34.3		46.1	16.7	24.5	52.0	46.0	44.1	13.7	15.7	69.8	44.8	41.7	47.0	85.2	47.1	6
7	54.5	50.5	56.3	60.5	52.5	48.5		21.2	19.2	45.6	34.0	98.1	19.2	14.4	49.0	35.6	28.6	41.0	74.1	61.5	7
8	75.0	77.7	76.3	80.0	77.2	72.8	71.0		24.0	19.4	21.0	21.2	24.0	66.3	14.6	16.1	14.3	20.0	22.2	18.3	8
9	73.5	71.0	73.7	78.6	77.6	71.4	73.7	68.3		22.3	19.0	17.3	23.8	21.2	20.8	16.1	16.7	20.0	37.0	22.1	9
10	42.6	43.7	31.1	68.2	46.5	45.5	52.4	72.0	72.7		40.0	44.7	17.5	14.6	55.2	41.4	34.5	37.0	85.2	49.5	10
11	55.2	53.1	55.1	58.8	55.2	47.9	54.5	70.3	71.9	53.1		34.0	16.0	16.0	41.7	72.4	45.2	50.0	44.4	33.0	11
12	55.4	52.4	56.3	60.5	53.5	50.5	1.9	71.0	75.8	53.4	54.5		18.3	14.4	47.9	34.5	28.6	42.0	70.4	61.5	12
13	73.1	75.8	74.5	79.7	80.6	77.4	72.3	67.0	69.5	72.3	76.9	73.4		21.2	11.5	12.6	10.7	14.0	33.3	15.4	13
14	80.4	81.9	76.3	81.2	81.5	80.4	74.2	33.7	73.1	77.4	76.9	74.2	72.0		13.5	13.8	14.3	15.0	22.2	15.4	14
15	46.3	41.7	48.4	60.0	37.9	27.4	48.4	76.7	73.9	45.3	47.8	49.5	81.6	84.9		47.1	35.7	40.6	74.1	50.0	15
16	54.2	54.1	54.1	61.2	55.4	50.6	57.0	74.7	74.7	51.8	27.6	58.1	79.5	83.5	44.0		44.0	41.4	33.3	31.0	16
17	55.6	56.6	61.4	67.5	59.3	55.6	68.7	80.8	81.9	59.0	56.0	68.7	87.2	83.3	58.5	54.4		56.0	25.9	35.7	17
18	51.0	56.1	58.2	59.5	51.0	45.8	53.5	75.3	69.1	56.1	42.9	52.5	77.5	78.7	48.9	51.8	40.2		44.4	46.0	18
19	11.1	11.1	14.8	57.1	18.5	14.8	25.9	68.0	51.9	14.8	37.5	29.6	55.6	72.0	13.0	35.7	57.9	41.7		81.5	19
20	50.5	52.4	53.4	61.6	45.5	49.5	38.5	71.0	73.7	48.5	57.6	38.5	75.5	74.2	48.4	62.8	61.4	48.5	18.5		20
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	

1 EG3IN.PRO
2 FUSEQIN.PRO
3 GLIOIN.PRO
4 ACRHYPO.PRO
5 ASPKAWA1.PRO
6 ASPACU1.PRO
7 HUMIN.PRO
8 11AG8IN.PRO
9 ERWCARIN.PRO
10 GLIO314.PRO
11 GLIO3HYP.PRO
12 HGRIS.PRO
13 RHMARIN.PRO
14 SLIVIN.PRO
15 PENNOT.PRO
16 PHANHYPO.PRO
17 F42HYPO.PRO
18 EMDESHYP.PRO
19 MYCINS.PRO
20 CHBRAS.PRO

FIGURE 4

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	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20		
1		51.0	52.9	27.0	49.0	56.9	43.1	17.6	18.6	55.9	37.0	42.2	16.7	14.7	50.0	39.1	36.9	36.0	88.9	46.1	1	EG3IN.PRO
2	43.1		48.5	22.5	47.1	55.9	43.3	15.4	21.2	54.4	37.0	41.3	15.4	13.5	55.2	40.2	34.5	34.0	88.9	42.3	2	FUSEQIN.PRO
3	42.6	48.5		21.3	42.2	49.0	41.7	15.5	22.3	68.9	38.0	41.7	16.5	12.6	50.0	40.2	34.5	33.0	85.2	44.7	3	GLIOIN.PRO
4	66.7	66.3	70.6		25.8	31.5	31.5	18.0	20.2	22.5	34.8	31.5	12.4	16.9	28.1	33.3	28.6	33.7	22.2	29.2	4	ACRHYPO.PRO
5	44.6	51.0	53.5	63.1		65.7	40.2	12.7	22.5	51.0	38.0	39.2	11.8	12.7	59.4	41.4	36.9	40.0	81.5	49.0	5	ASPKAWA1.PRO
6	36.6	41.2	46.5	61.9	34.3		46.1	16.7	24.5	52.0	46.0	44.1	13.7	15.7	69.8	44.8	41.7	47.0	85.2	47.1	6	ASPACU1.PRO
7	54.5	50.5	56.3	60.5	52.5	48.5		21.2	19.2	45.6	34.0	98.1	19.2	14.4	49.0	35.6	28.6	41.0	74.1	61.5	7	HUMIN.PRO
8	75.0	77.7	76.3	80.0	77.2	72.8	71.0		24.0	19.4	21.0	21.2	24.0	66.3	14.6	16.1	14.3	20.0	22.2	18.3	8	11AG8IN.PRO
9	73.5	71.0	73.7	78.6	77.6	71.4	73.7	68.3		22.3	19.0	17.3	23.8	21.2	20.8	16.1	16.7	20.0	37.0	22.1	9	ERWCARIN.PRO
10	42.6	43.7	31.1	68.2	46.5	45.5	52.4	72.0	72.7		40.0	44.7	17.5	14.6	55.2	41.4	34.5	37.0	85.2	49.5	10	GLIO314.PRO
11	55.2	53.1	55.1	58.8	55.2	47.9	54.5	70.3	71.9	53.1		34.0	16.0	16.0	41.7	72.4	45.2	50.0	44.4	33.0	11	GLIO3HYP.PRO
12	55.4	52.4	56.3	60.5	53.5	50.5	1.9	71.0	75.8	53.4	54.5		18.3	14.4	47.9	34.5	28.6	42.0	70.4	61.5	12	HGRIS.PRO
13	73.1	75.8	74.5	79.7	80.6	77.4	72.3	67.0	69.5	72.3	76.9	73.4		21.2	11.5	12.6	10.7	14.0	33.3	15.4	13	RHMARIN.PRO
14	80.4	81.9	76.3	81.2	81.5	80.4	74.2	33.7	73.1	77.4	76.9	74.2	72.0		13.5	13.8	14.3	15.0	22.2	15.4	14	SLIVIN.PRO
15	46.3	41.7	48.4	60.0	37.9	27.4	48.4	76.7	73.9	45.3	47.8	49.5	81.6	84.9		47.1	35.7	40.6	74.1	50.0	15	PENNOT.PRO
16	54.2	54.1	54.1	61.2	55.4	50.6	57.0	74.7	74.7	51.8	27.6	58.1	79.5	83.5	44.0		44.0	41.4	33.3	31.0	16	PHANHYPO.PRO
17	55.6	56.6	61.4	67.5	59.3	55.6	68.7	80.8	81.9	59.0	56.0	68.7	87.2	83.3	58.5	54.4		56.0	25.9	35.7	17	F42HYPO.PRO
18	51.0	56.1	58.2	59.5	51.0	45.8	53.5	75.3	69.1	56.1	42.9	52.5	77.5	78.7	48.9	51.8	40.2		44.4	46.0	18	EMDESHYP.PRO
19	11.1	11.1	14.8	57.1	18.5	14.8	25.9	68.0	51.9	14.8	37.5	29.6	55.6	72.0	13.0	35.7	57.9	41.7		81.5	19	MYCINS.PRO
20	50.5	52.4	53.4	61.6	45.5	49.5	38.5	71.0	73.7	48.5	57.6	38.5	75.5	74.2	48.4	62.8	61.4	48.5	18.5		20	CHBRAS.PRO
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20		

PERCENT DIVERGENCE

PERCENT SIMILARITY

FIG._4

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FIGURE 6

```
                         1                                                          60
T._reesei                M.........KF.LQVLPALIPAALAQTS...............CDQWATFTGNG..YTV
H._schweinitzii          M.........KF.LQVLPAILPAALAQTS...............CDQYATFSGNG..YIV
A._aculeatus__           M.........KAFHL.LAALAGAAVAQQAQ............LCDQYATYTGGV..YTI
A._kawachii__            M.........KLSMT.LSLFAATAMGQT...............MCSQYDSASSPP..YSV
A._kawachii_2            M.........KAFHL.LAALSGAAVAQQAQ............LCDQYATYTGGV..YTI
A._oryzae__              M.........KLSLA.LATLVATAFSQE...............LCAQYDSASSPP..YSV
H._grisei                M........LKSALLLGAAAVSVQSASIPTIPANLEPRQIR.SLCELYGYWSGNG..YEL
H._insolens__            M........LKSALLLGPAAVSVQSASIPTIPANLEPRQIR.SLCELYGYWSGNG..YEL
Chaetomium_brasiliense   M.........KLTLVLFVSSLA......AATPLGWRERQQQVSLCGQSSSWSGNG..YQL
F._equseti               M.........KSTLLLAGAFAPLAFAKD...............LCEQYGYLSSDG..YSL
F._javanicum_1           M.........KSAIVA.ALAGLAAASPTRLIPRGQ........FCGQWDSETAGA..YTI
F._javanicum_2           M.........K..FFGVVSASLAATAVATPTTPTETIEKRDTTWCDAFGSLATSG..YTV
G._roseum____1           M.........KANIVILSLFAPLAAVAQT..............LCGQYSSNTQGG..YIF
G._roseum____2           M.........KSIISFFGLATLVAAAPSQNPTRTQPLEKRATTLCGQWDSVETGG..YTI
G._roseum____3           M.........KFQLLSLTAFAPLSLAA................LCGQYQSQSQGG..YIF
G._roseum____4           M.........KTGIAYLAAVLPLA.MAES..............LCDQYAYLSRDG..YNF
Memnoniella_echinata     M.........KVAAL.LVALSPLAF.AQS..............LCDQYSYYSSNG..YEF
Emericella_desertoru     M.........K..LLALSLVSLASAASAASIL.SNTFTRRSD.FCGQWDTATVGN..FIV
Actinomycete_11AG8       MRS......HPRS..ATM.TVLVVLASLGALLTAAAPAQANQQICDRYGTTTIQD.RYVV
S._lividans_CelB__       MRTLRPQARAPRGLLAALGAVLAAFALVSSLVTAAAPAQADTTICEPFGTTTIQG.RYVV
Rhodothermus_marinus__   MNVMR..AVLVLSLLLLFGCDWL.FPDGDNGKEPEPEPEPTVELCGRWDARDVAGGRYRV
Erwinia_carot___         MQTVNTQPHRIFRVLLPAVFSSLLLSSLTVSAASSSNDADKLYF.........GNNKYYL

                         61                                                        120
T._reesei                SNNLWGASAGSGF..GCV.TAVSLSGG.ASWHADWQWSGGQNNVKSYQNS..........
H._schweinitzii          SNNLWGASAGSGF..GCV.TSVSLNGA.ASWHADWQWSGGQNNVKSYQNV..........
A._aculeatus__           NNNLWGKDAGSG..SQCTTVNSASSAG.TSWSTKWNWSGGENSVKSYANS..........
A._kawachii__            NQNLWGEYQGTG..SQCVYVDKLSSSG.ASWHTKWTWSGGEGTVKSYSNS..........
A._kawachii_2            NNNLWGKDAGSG..SQCTTVNSASSAG.TSWSTKWNWSGGENSVKSYANS..........
A._oryzae__              NNNLWGQDSGTGFTSQCVYVDNLSSSG.AAWHTTWTWNGGEGSVKSYSNS..........
H._grisei                LNNLWGKDTATS.GWQCTYLDGTNNGG.IQWNTAWEWQGAPDNVKNYPYV..........
H._insolens__            LNNLWGKDTATS.GWQCTYLDGTNNGG.IQWSTAWEWQGAPDNVKSYPYV..........
Chaetomium_brasiliense   NNNLWGQSRATS.GSQCTYLDSSSNSG.IHWHTTWTWEGGEGEVKSYAYS..........
F._equseti               NNNVWGKDSGTGD..QCTHVNWNNANG.AGWDVEWNWSGGKDNVKSYPNS..........
F._javanicum_1           YNNLWGKDNAES.GEQCTTNSGEQSDGSIAWSVEWSWTGGQGQVKSYPNA..........
F._javanicum_2           YHNNWGKGDATS.GSQCTTFTSVSNNNFV.WSTSWTWAGGAGKVKSYSNV..........
G._roseum____1           NNNMWGMGSGSGS..QCTYVDKVWAEG.VAWHTDWSWSGGDNNVKSYPYS..........
G._roseum____2           YNNLWGQDNG.S.GSQCLTVEGV.TDGLAAWSSTWSWSGGSSSVKSYSNA..........
G._roseum____3           NNNKWGQGSGSGS..QCLTIDKTWDSN.VAFHADWSWSGGTNNVKSYPNA..........
G._roseum____4           NNNEWGAATGTGD..QCTYVDSTSSGG.VSWHSDWTWSGSESEIKSYPYS..........
Memnoniella_echinata     NNNMWGRNSGQGN..QCTYVDYSSPNG.VGWRVNWNWSGGDNNVKSYPYS..........
Emericella_desertoru     YNNLWGQDNADS.GSQ..TGVDSANGNSISWHTTWSWSGGSSSVKSYANA..........
Actinomycete_11AG8       QNNRWGTSAT.....QCINVT..GNGFEITQADGS..VPTNGAPKSYPSVYDGCHYG...
S._lividans_CelB__       QNNRWGSTAP.....QCVTAT..DTGFRVTQADGS..APTNGAPKSYPSVFNGCHYT...
Rhodothermus_marinus__   INNVWGAETA.....QCIEVGLETGNFTITRADHD..NGNNVA..AYPAIYFGCHWAPAR
Erwinia_carot___         FNNVWGKDEIKGWQQTIFYNSPISMG....WN..WHWPSSTHSVKAYPSLVSGWHWTAG.

                         121                                                       180
T._reesei                .QIAIP.QKRTVNSISSMPTTASW...SYSGSNIRANVAYDL.FTAANPNHVTYSGDYEL
H._schweinitzii          .QINIP.QKRTVNSIGSMPTTASW...SYSGSDIRANVAYDL.FTAANPNHVTYSGDYEL
A._aculeatus__           .GLTF..NKKLVSQISQIPTTARW.S..YDNTGIRADVAYDL.FTAADINHVTWSGDYEL
A._kawachii__            .GLTF..DKKLVSDVSSIPTSVTW.SQD..DTNVQADVSYDL.FTAANADHATSSGDYEL
A._kawachii_2            .GLSF..NKKLVSQISHIPTAARW.S..YDNTCIRRGRAYDL.FTAADINHVTWSGDYEL
A._oryzae__              .AVTF..DKKLVSDVQSIPTDVEW.SQDFTNTNVNADVAYDL.FTAADQNHVTYSGDYEL
H._grisei                .GKQIQRGRK.ISDINSMRTSVSW...TYDRTDLRANVAYDV.FTARDPDHPNWGGDYEL
H._insolens__            .GKQIQRGRK.ISDINSMRTSVSW...TYDRTDIRANVAYDV.FTARDPDHPNWGGDYEL
Chaetomium_brasiliense   .GRQVSTGLT.IASIDSMQTSVSW...EYNTTDIQANVAYDI.FTAEDPDHEHSSGDYEL
F._equseti               .ALLIGEDKKTISSITNMQSTAEW...KYSGDNLRADVAYDL.FTAADPNHETSSGEYEL
F._javanicum_1           .VVEI..EKKTLGEVSSIPSA..W.DWTYTGNGIIANVAYDL.FTSSTESGDA...EYEF
F._javanicum_2           .ALEK..INKKISDIKSVSTR..W.IWRYTGTKMIANVSYDL.WFAPTASSNN...AYEI
G._roseum____1           .GRELGT.KRIVSSIKSISSGADW...DYTGSNLRANAAYDI.FTSANPNHATSSGDYEV
G._roseum____2           .VLSA..EAARISAISSIPSK..W.EWSYTGTDIVANVAYDL.FSNTDCGDTP...EYEI
G._roseum____3           .GLEFSR.GKKVSSIGTINGGADW...DYSGSNIRANVAYGI.FTSADPNHVTSSGDYEL
G._roseum____4           .GLDLPE.KKIVTSIGSISTGAEW...SYSGSDIRADVAYDT.FTAADPNHATSSGDYEV
Memnoniella_echinata     .GRQLPT.KRIVSWIGSLPTTVSW...NYQGNNLRANVAYDL.FTAANPNHPNSSGDYEL
Emericella_desertoru     .AYQF..TSTKLNSLSSIPTS..W.KWQYSTTDIVANVAYDL.FTSSSAGGDS...EYEI
Actinomycete_11AG8       ...NCAPRTTLPMRISSIGSAPSSVSYRYTGNGVY.NAAYDIWLDPTPRTNGVNR..TEI
S._lividans_CelB__       ...NCSPGTDLPVRLDTVSAAPSSISYGFVDGAVY.NASYDIWLDPTARTDGVNQ..TEI
Rhodothermus_marinus__   AIRDCAARAGAVRRAHELDVTP.......ITTGRW.NAAYDIWFSPVTNSGNGYSGGAEL
Erwinia_carot___         ....YTENSGLPIQLSSNKSITSNVTYSIKATGTY.NAAYDIWFHTTDKANWDSSPTDEL

                         181                                                       240
T._reesei                MIWLGKYGDIGPIGSS....QGTVNVGGQSWTLYYGYNGAMQV......YSFVAQT.NTT
H._schweinitzii          MIWLGKYGDIGPIGSS....QGTVNVGGQTWTLYYGYNGAMQV......YSFVAQS.NTT
A._aculeatus__           MIWLARYGGVQPIGSQ....IATATVDGQTWELWYG......ANGSQKTYSFVAPT.PIT
A._kawachii__            MIWLARYGSVQPIGKQ....IATATVGGKSWEVW..YGTSTQAGAEQKTYSFVAGS.PIN
A._kawachii_2            MIWLARYGGVQPLGSQ....IATATVEGQTWELWYG......VNGAQKTYSFVAAN.PIT
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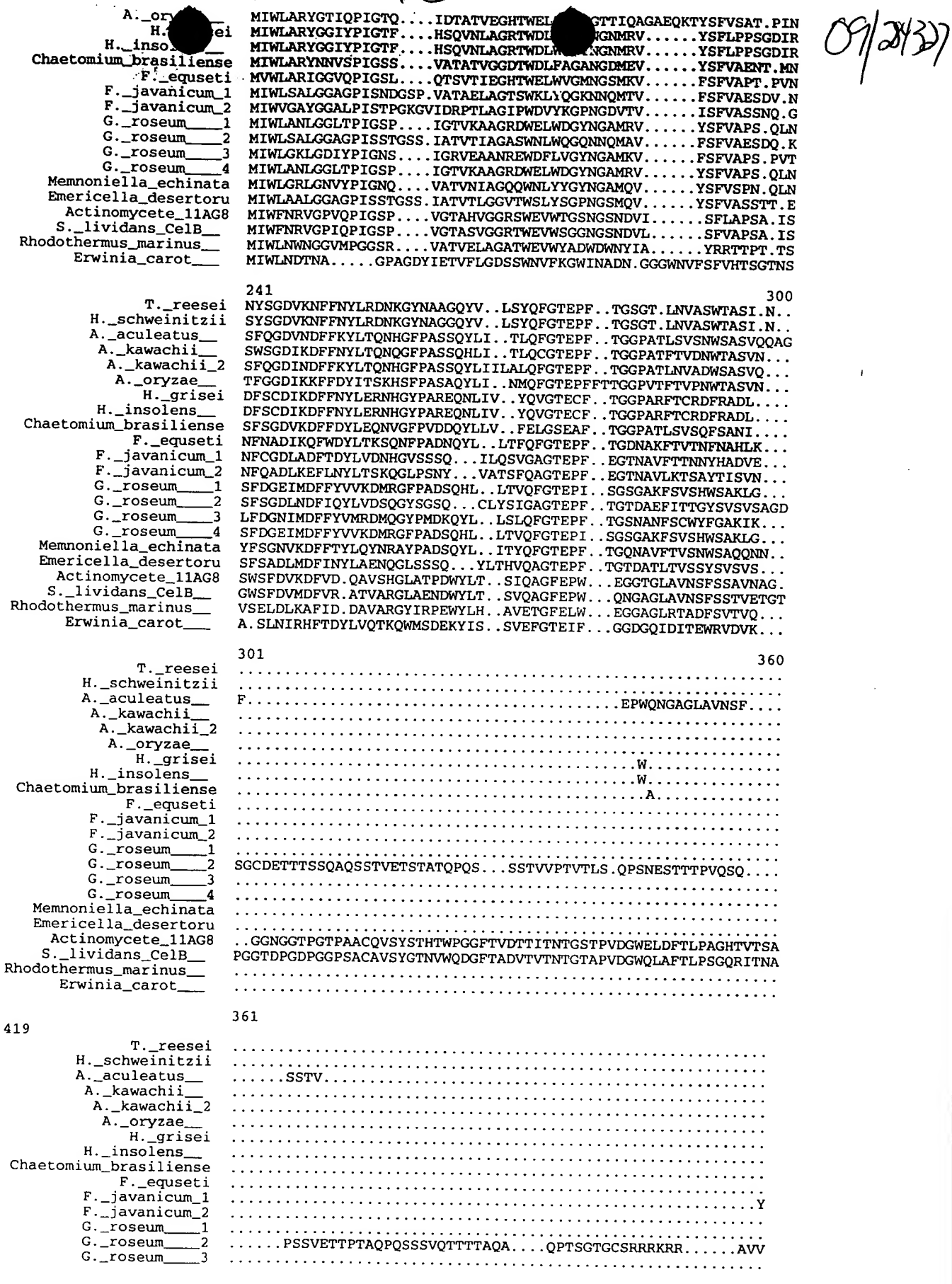

Fig 6 (continued)

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G._roseu[illegible]_4          ............................................................
Memnoniella_ec[illegible]a     ............................................................
Emericella_des[illegible]u     ............................................................
Actinomycete_[illegible]AG8    WNALISPASGAVTARSTGSNGRIAANGGTQSFGFQG[illegible]SSGTGFNAPAGGRLNGTSCTVR
S._lividans_CelB__             WNASLTPSSGSVTATGASHNARIAP.GGSLSFGFQGTYGGA.FAEPTGFRLNGTACTTV
Rhodothermus_marinus__         ............................................................
Erwinia_carot___               ............................................................
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Fig 6 (Continued)